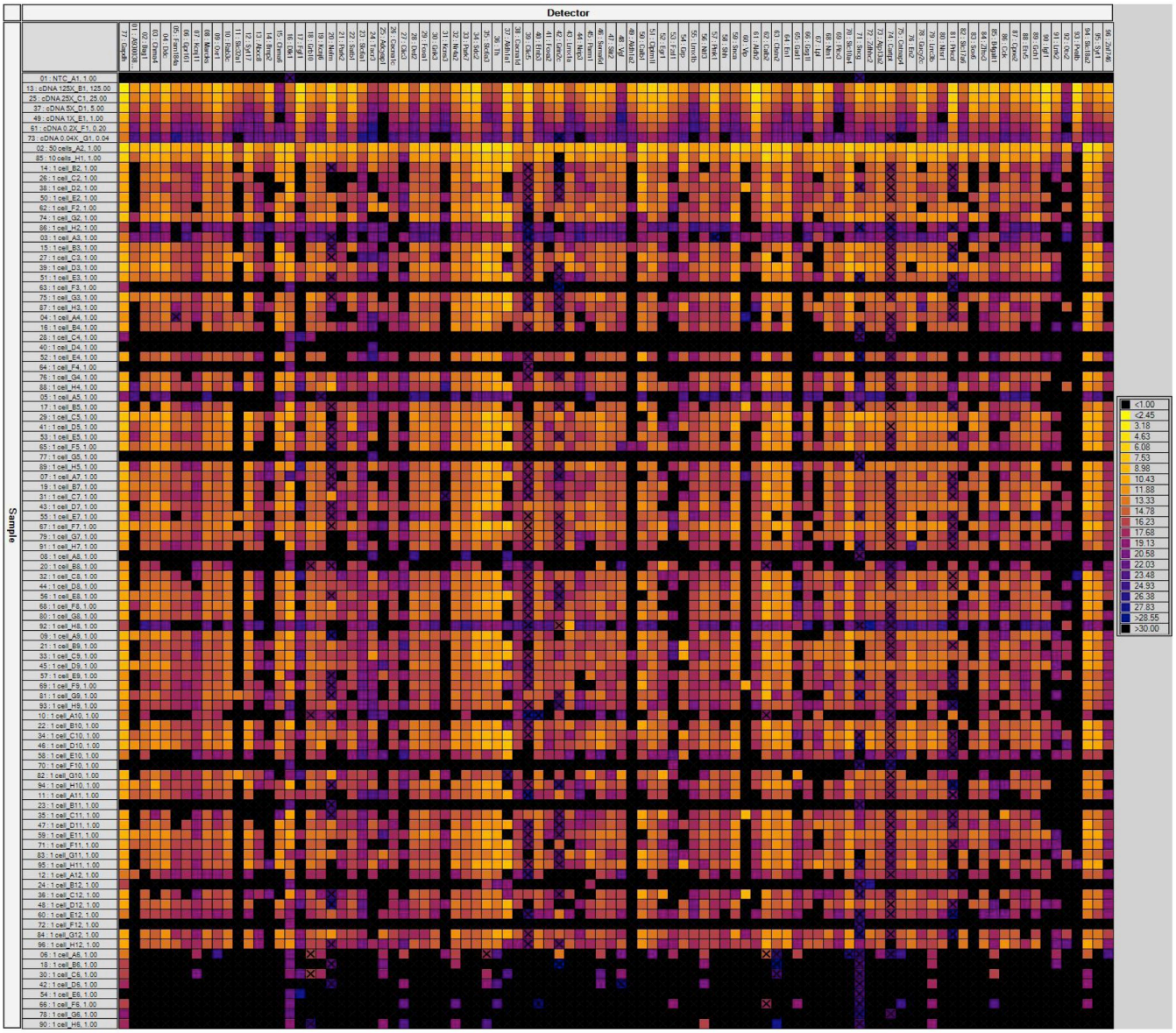
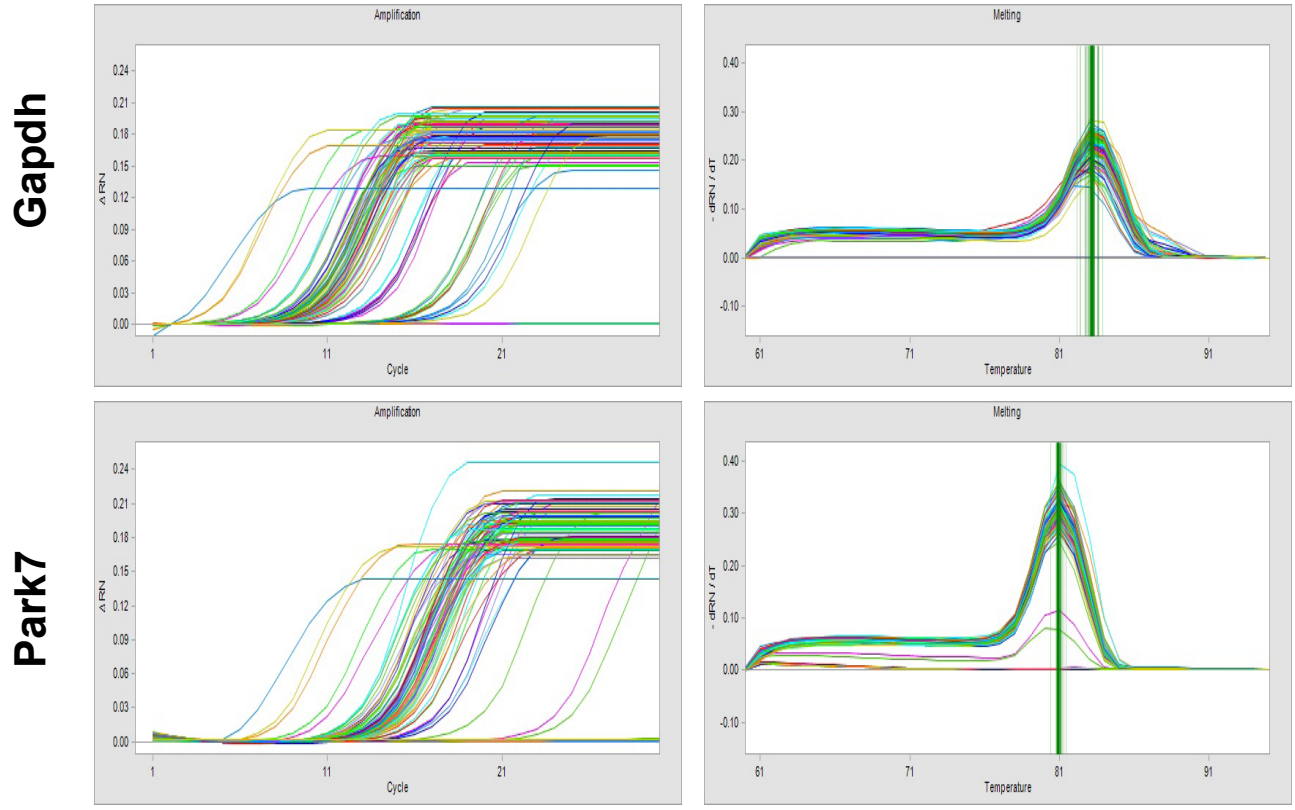
Supplemental information inventory

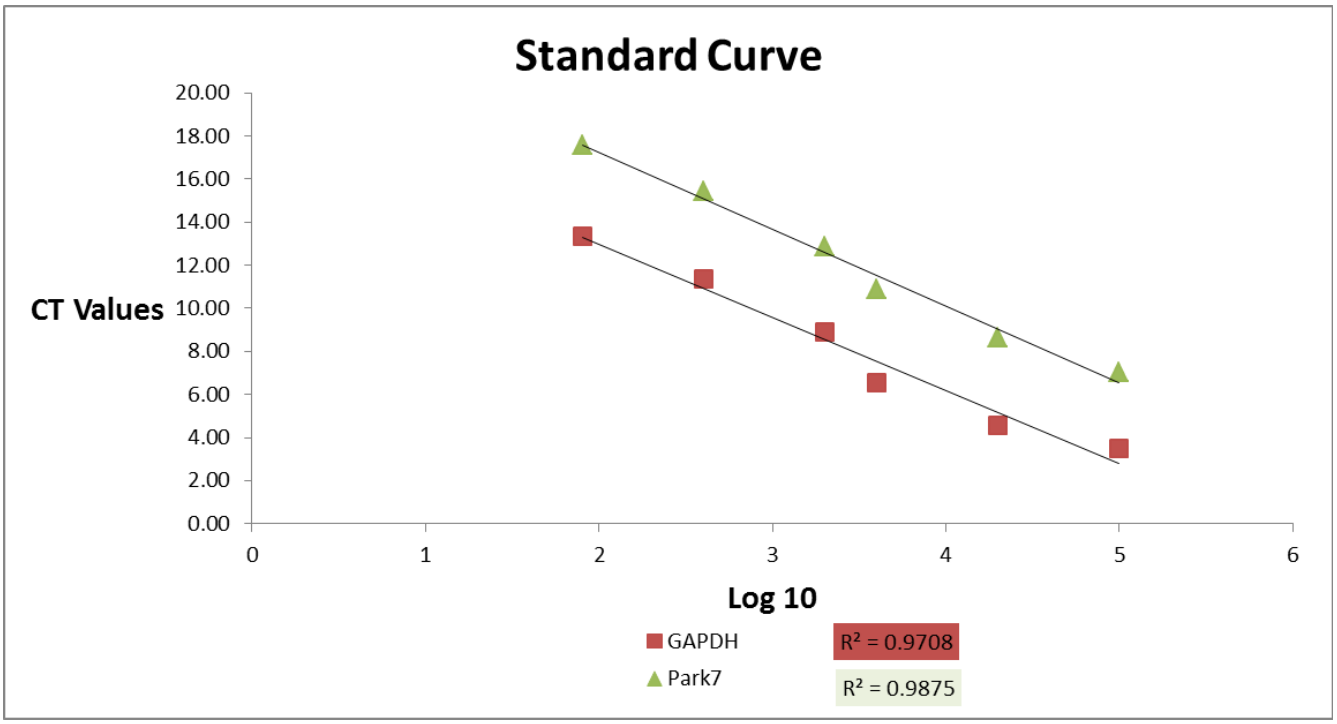
Figure S1. Microfluidic chip cycle threshold (Ct) output values (Related to Fig. 1)



The midbrain of a Slc6a3::Cre; Ai9 P4 mouse was carefully dissected and dissociated using Papain Dissociation System (Worthington Biochemical Corporation). Single cell expressing tdTomato were immediately sorted in a 96-well (Fig. 1). In the first experiment, 87 single cells were sorted for gene expression analysis (row 10 to 96), 9 wells were used for whole brain cDNA dilution to generate calibration curves (row 2 to 7), and finally a 10 cells and 50 cells positive controls (row 8 and 9) and a negative control (row 1). The expression of each of the 96 genes was quantitatively evaluated for each of these cells. In addition, despite showing a normal standard curve, two genes *Pvalb* and *Bmp2* were undetectable in all cells analyzed, and these genes were thus excluded from further analysis. For quality control, the melt curve was established and all peaks falling outside user-defined threshold was removed from analysis (square with black “X”).

Figure S2. Example of qPCR output and quality control (Related to Fig. 1)





Example of data generated in Fig. 1.

Figure S3. Complete expression profile (Related to Fig. 1)

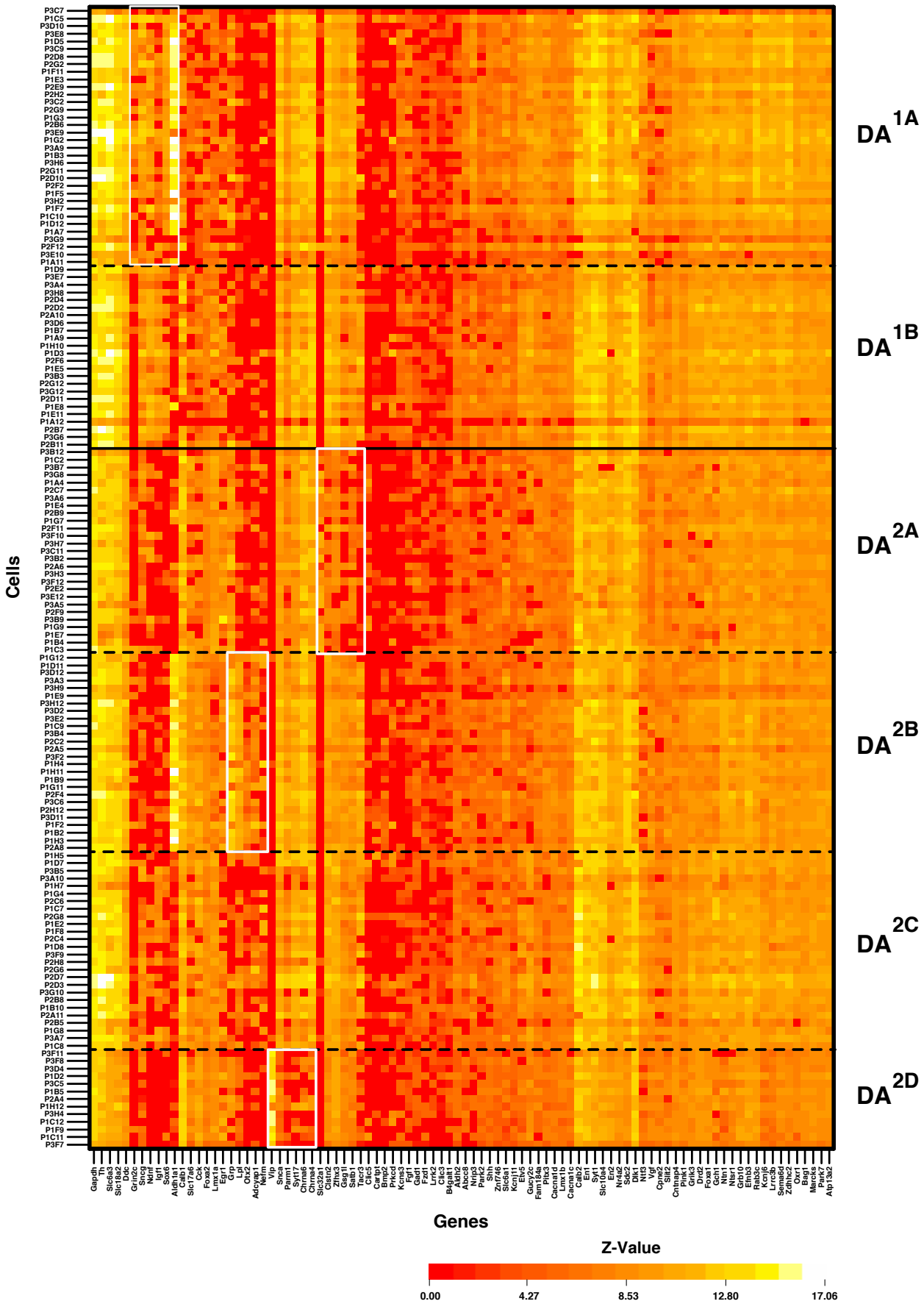


Figure S4. Hierarchical cluster analysis (Related to Fig. 1)

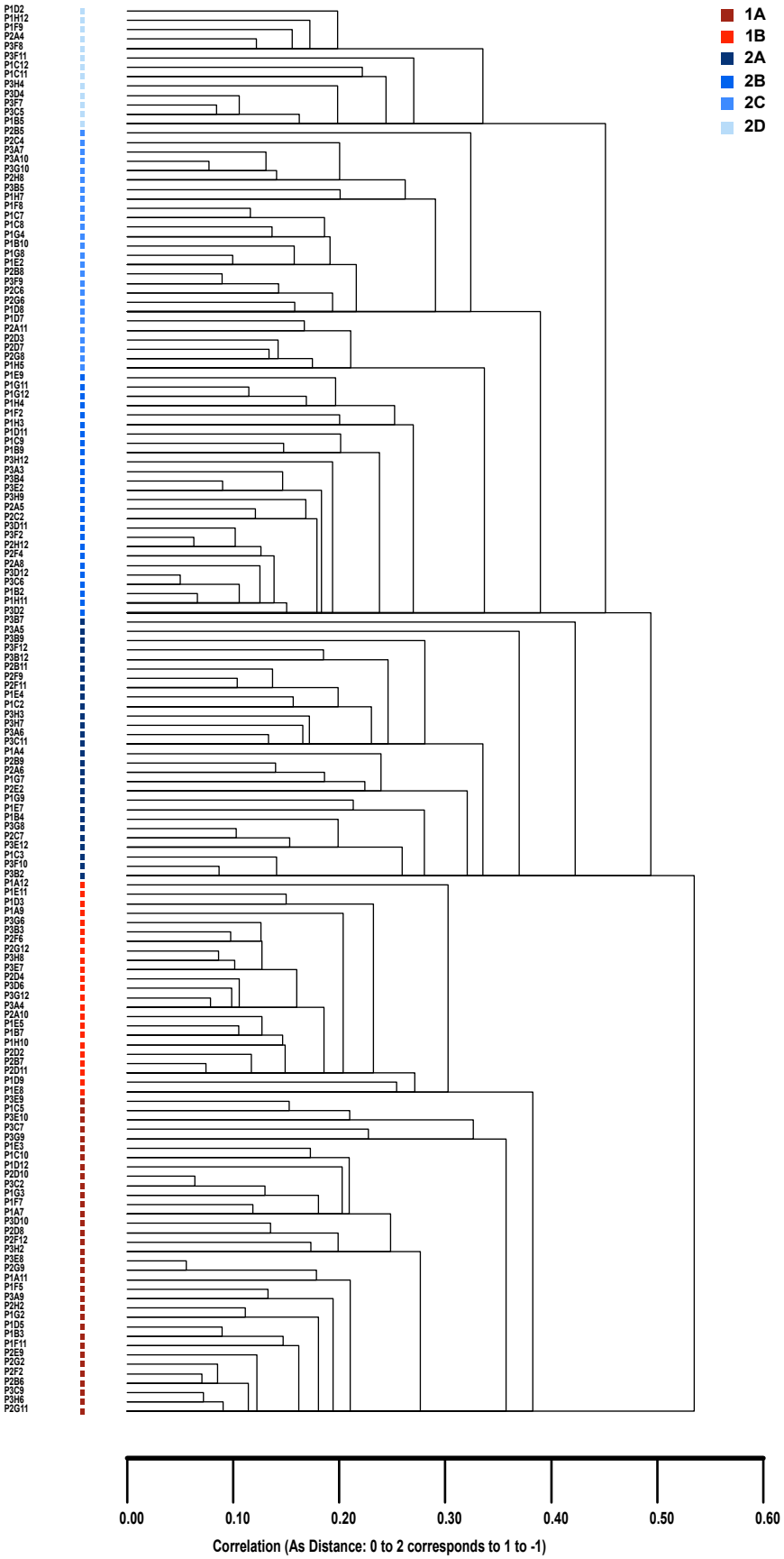
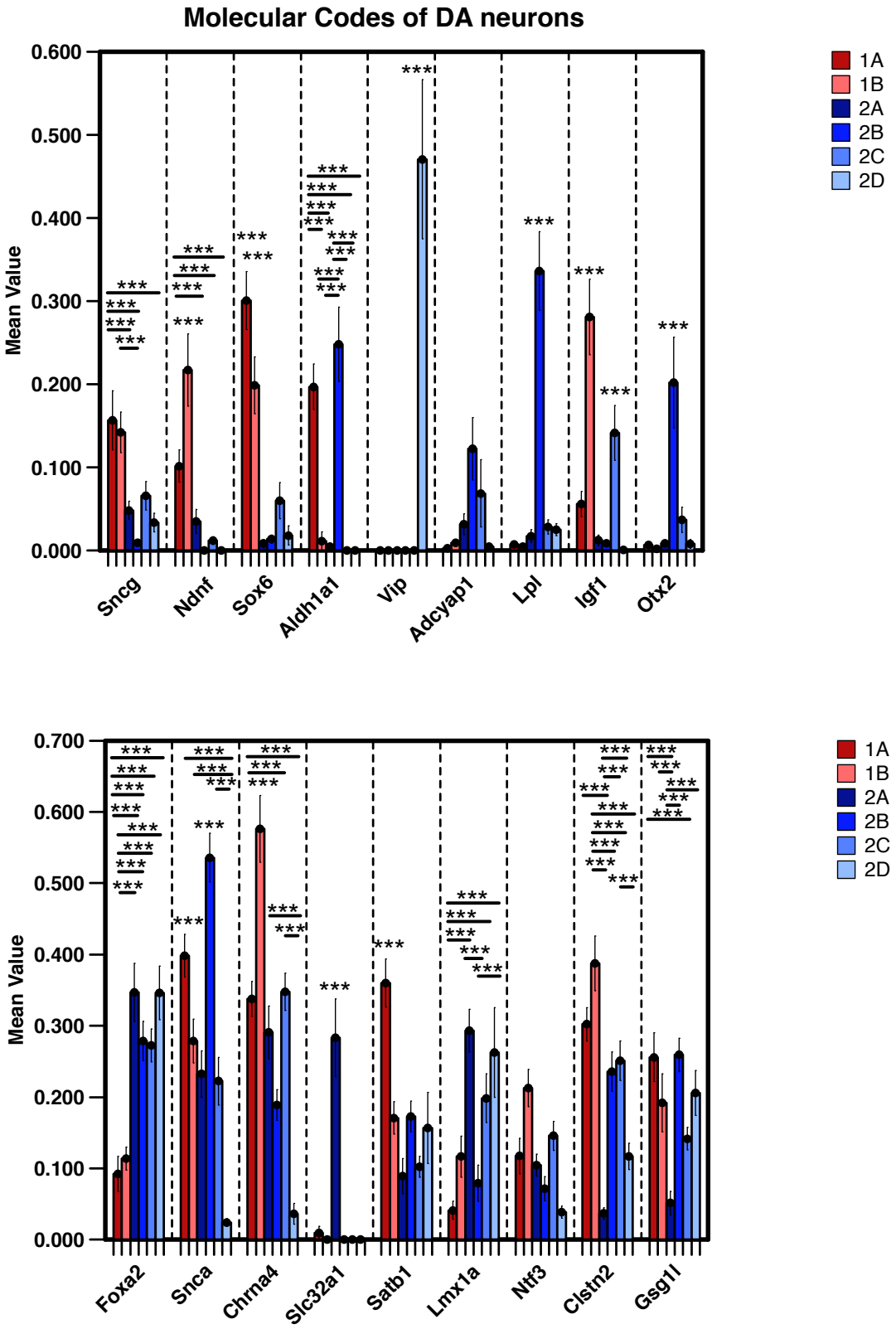
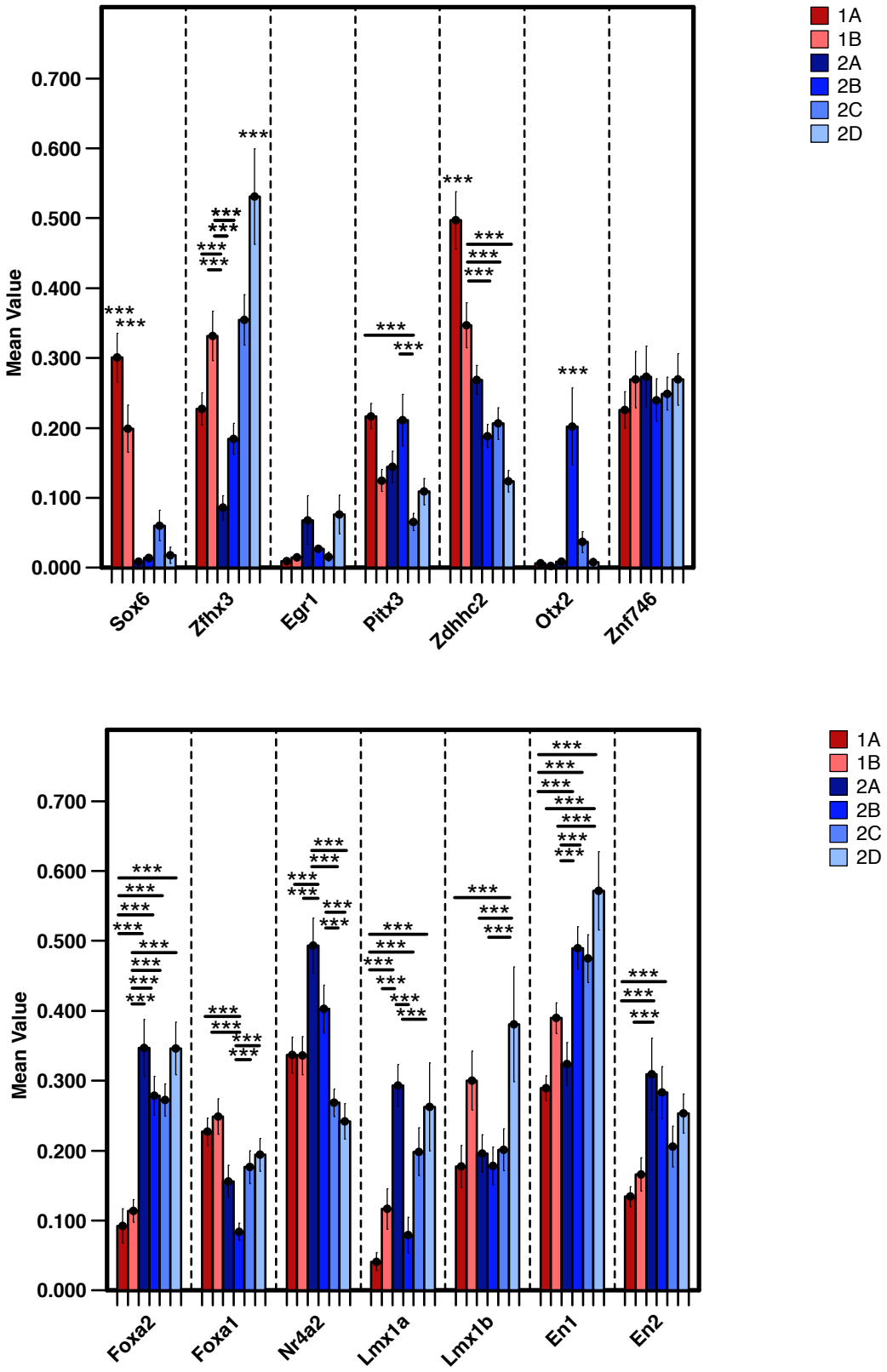


Figure S5. Complete statistical analysis of single-cell gene expression (Related to Fig. 3)

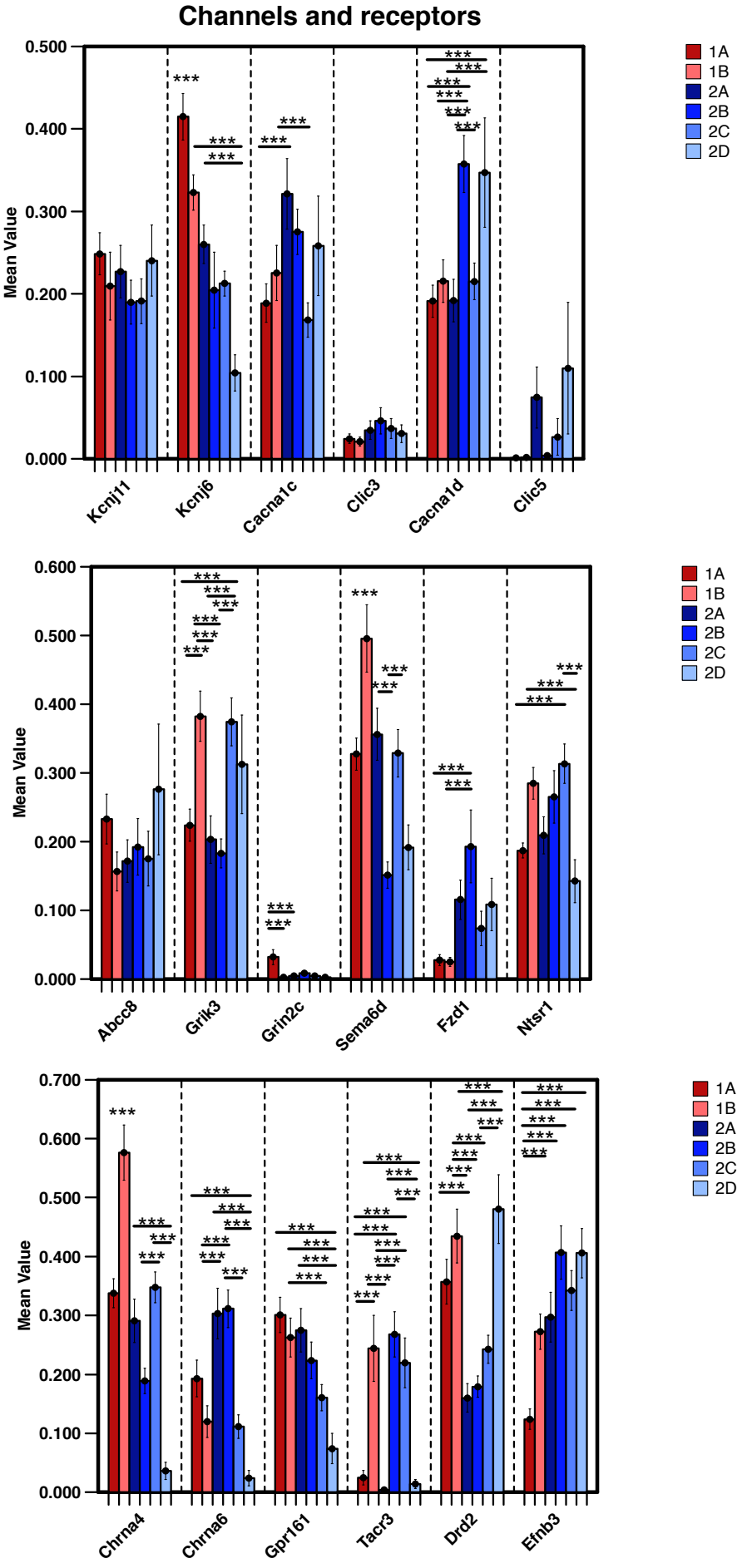
a



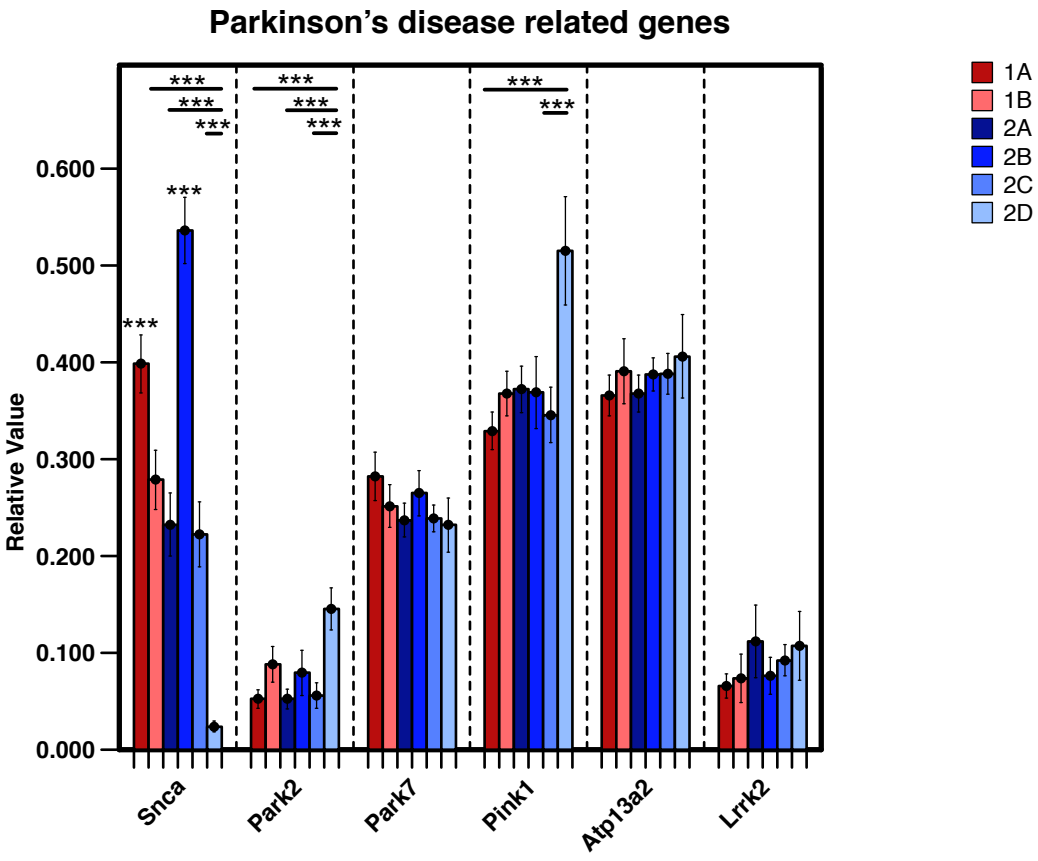
b


Transcription factors
Mean Value
0.000
0.100
0.200
0.300
0.400
0.500
0.600
0.700
1A
1B
2A
2B
2C
2D
Sox6
Zfhx3
Egr1
Pitx3
Zdhhc2
Otx2
Znf746
Foxa2
Foxa1
Nr4a2
Lmx1a
Lmx1b
En1
En2

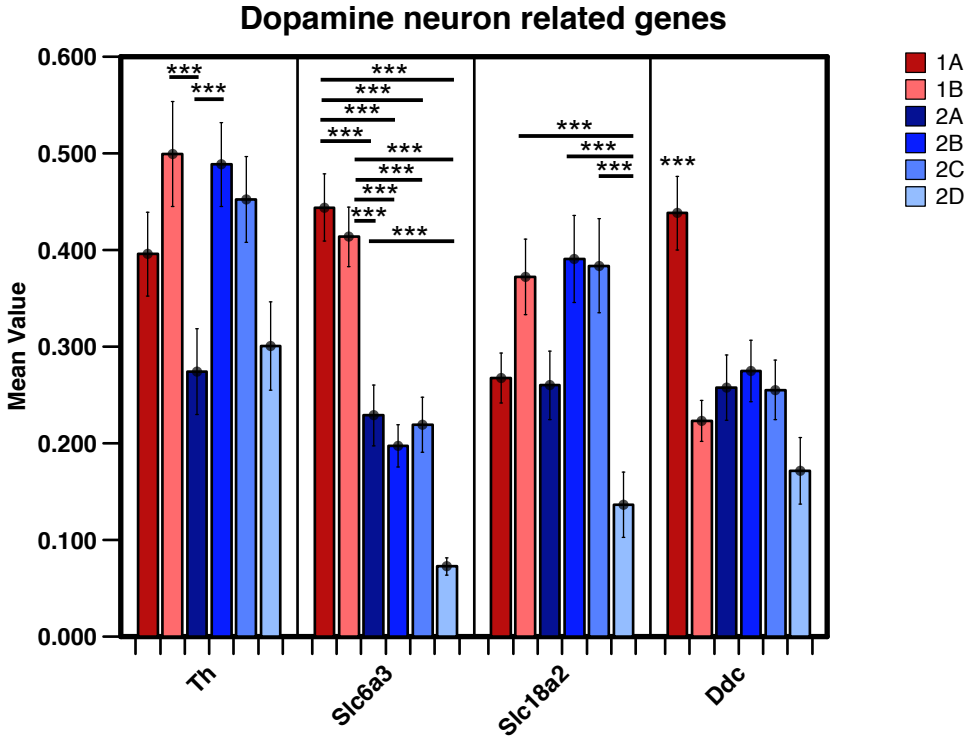
c


Channels and receptors
Mean Value
0.500
0.400
0.300
0.200
0.100
0.000
Kcnj11
Kcnj6
Cacna1c
Clic3
Cacna1d
Clic5
1A
1B
2A
2B
2C
2D
0.600
0.500
0.400
0.300
0.200
0.100
0.000
Abcc8
Grik3
Grin2c
Sema6d
Fzd1
Ntsr1
0.700
0.600
0.500
0.400
0.300
0.200
0.100
0.000
Chrna4
Chrna6
Gpr161
Tacr3
Drd2
Efnb3

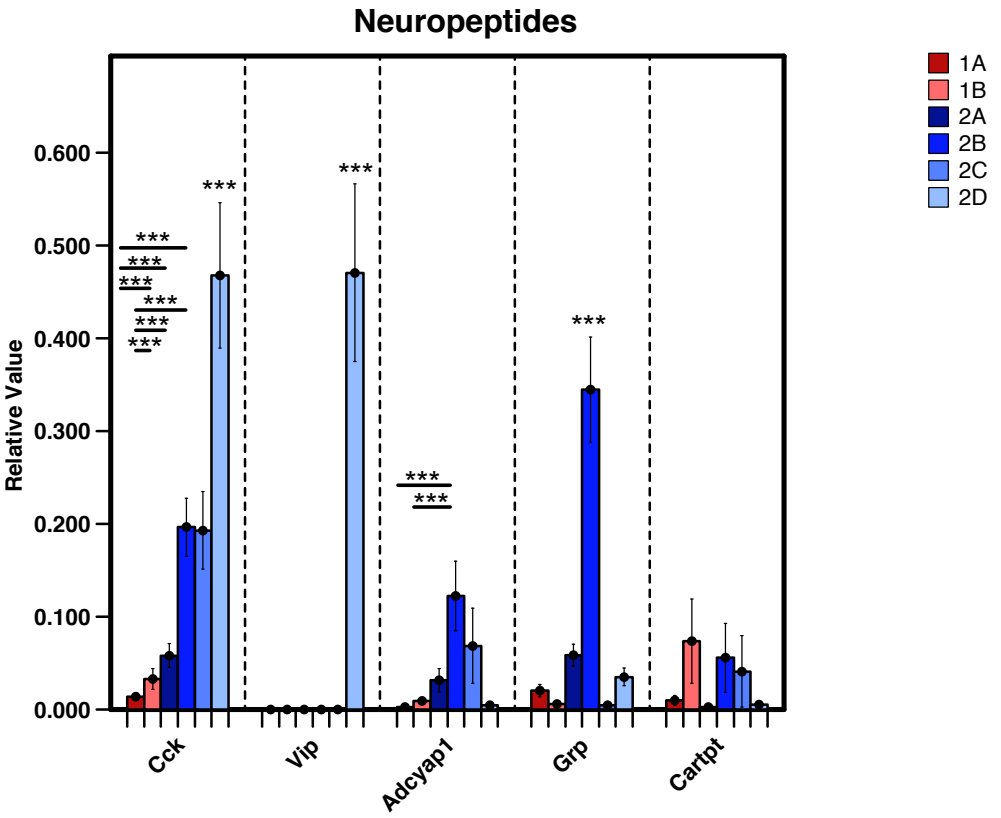
d


Parkinson's disease related genes
Relative Value
0.000
0.100
0.200
0.300
0.400
0.500
0.600
Snca
Park2
Park7
Pink1
Atp13a2
Lrrk2
1A
1B
2A
2B
2C
2D

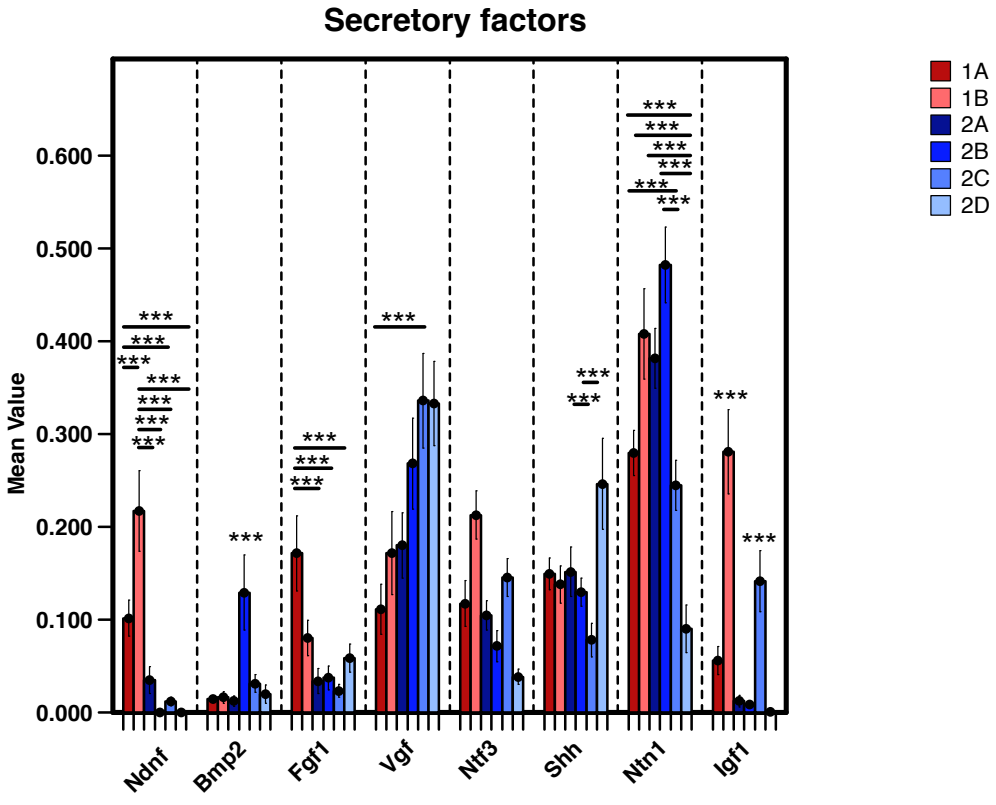
e


Dopamine neuron related genes
Mean Value
0.000
0.100
0.200
0.300
0.400
0.500
0.600
Th
Slc6a3
Slc18a2
Ddc
1A
1B
2A
2B
2C
2D

f

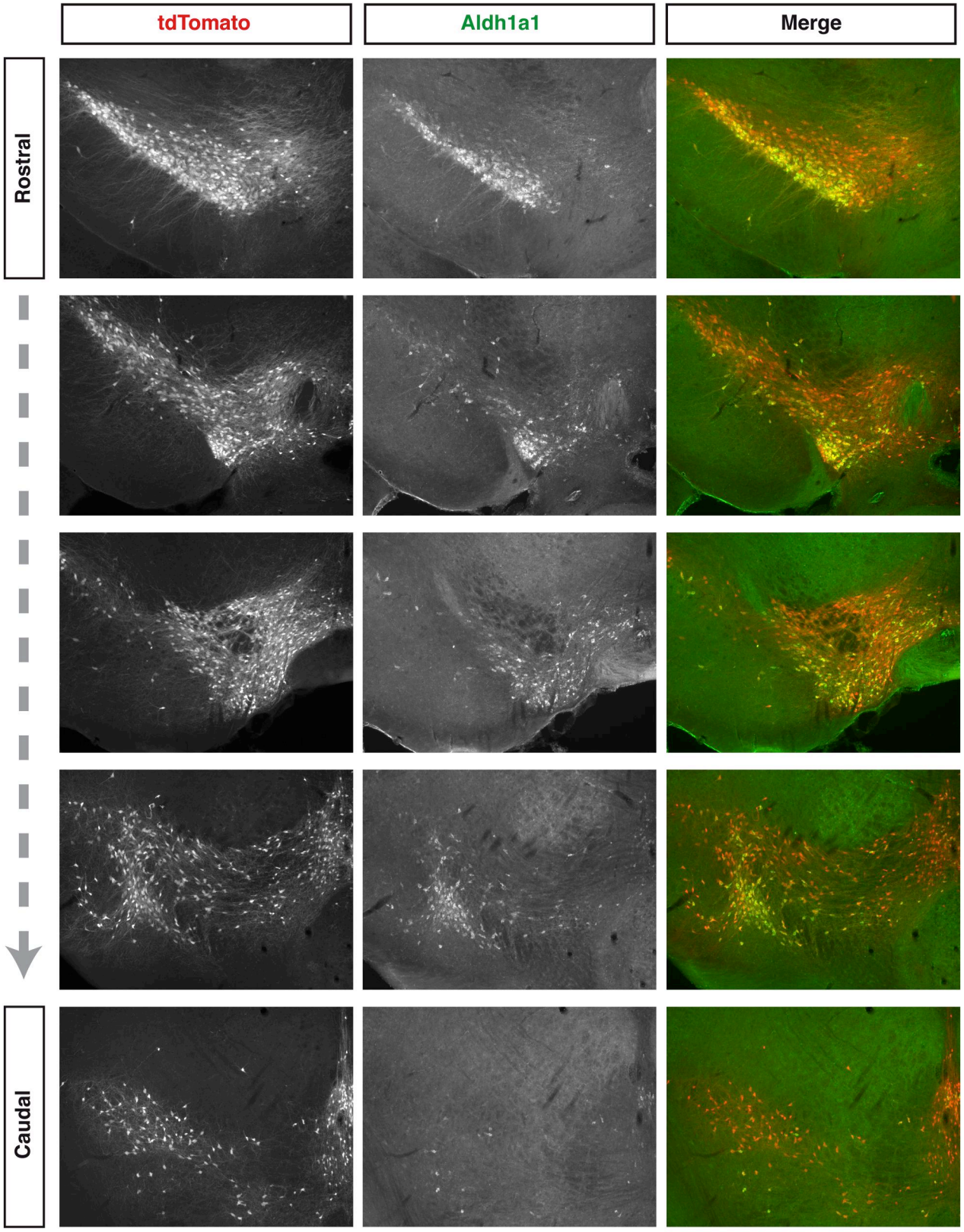


g



Statistical analysis of the single-cell gene expression data generated in the experiment described in Fig. 1. The Kruskal-Wallis analysis of normalized value is illustrated for key genes (**a**), transcription factors (**b**), channels and receptors (**c**), Parkinson's disease related genes (**d**), genes related to DA-neurons (**e**), neuropeptides (**f**), and secretory factors (**g**). Stars located directly over a column indicate it is significantly different to every other groups. *** = $p < 0.001$.

Figure S6. Rostrocaudal distribution of tdTomato and Aldh1a1 (Related to Fig. 3 and 6).



Slc6a3::Cre, Ai9 mouse (tdTomato) depicting the midbrain rostrocaudal distribution of Aldh1a1 as illustrated in Fig. 4.